

RESULT 2

AAH29768/c

ID AAH29768 standard; DNA; 731 BP.

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AC AAH29768;

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DT 27-JUL-2001 (first entry)

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DE *S cerevisiae* apoptosis associated coding sequence YGL235W.

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KW Yeast; fungus; apoptosis; infection; proliferative disease; vaccine;

KW autoimmune disease; ischaemia; neurodegeneration; ds.

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OS *Saccharomyces cerevisiae*.

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PN WO200102550-A2.

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PD 11-JAN-2001.

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PF 03-JUL-2000; 2000WO-BE000077.

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PR 01-JUL-1999; 99EP-00870141.

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PA (JANC ) JANSSEN PHARM NV.

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PI Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;

PI Nelissen BJM, Reekmans RJ;

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DR WPI; 2001-367042/38.

DR P-PSDB; AAG70732.

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PT Yeast and fungal nucleic acids encoding proteins involved in a pathway

PT leading to programmed cell death, useful for treating proliferative

PT disorders, yeast and fungal infections, or for preventing apoptosis in

PT certain diseases.

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PS Claim 1; Fig 1; 218pp; English.

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CC The present invention provides the protein and coding sequences of a

CC number of apoptosis associated proteins from the yeast *Saccharomyces*

CC *cerevisiae* and the fungus *Candida albicans*. These can be used to identify

CC treatments for fungal and yeast infections, for proliferative diseases

CC and for apoptosis related diseases such as autoimmune diseases, ischaemia

CC and neurodegeneration. The present sequence is one of the *S. cerevisiae*

CC coding sequences of the invention

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SQ Sequence 731 BP; 200 A; 147 C; 159 G; 225 T; 0 U; 0 Other;

Query Match 28.3%; Score 283.4; DB 4; Length 731;  
Best Local Similarity 81.0%; Pred. No. 1.3e-60;  
Matches 367; Conservative 0; Mismatches 81; Indels 5; Gaps 3;

Qy 551  
TTAGCAATACGCTTCTGAACGAGGATCTATAGCAACTAAATTCAGACATTCTG  
CTACACC 610

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Db 731 TTAACAATAAGCTTCTGTACGAGGGTCCAAATCTA--  
AAATTCGGATATTCTTTTGTACC 674

Qy 611  
AAAAATGGAAGTATCACAGGAACGGAAAAGGGTTTTATAAGGCACCTCGGC  
ACCCCTATA 670

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Db 673  
GAAAAAGGAAATGTACAGGCACAGAAAAGGGTTTTATAAGGCACCTCGGC  
A-CCCTATA 615

Qy 671  
ACTGGCATTCTCACATTCGGCGCATACGAATAGACAAAGGCCCCAGAAAACA  
ATACCTTC 730

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Db 614  
ATTGGCATTCCCACATTCTGCGCATACGAATACACATGAGTGCCATAATACA  
ATACTCCA 555

Qy 731  
GCATACAGAATCTATAAAGATGCATGCCTCGTTTAAAAACAAGAACATCTTC  
ATAGTGAT 790

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Db 554  
CATACGAAGTCTATGAAAGATGTATGATTCGTTTCAGAAACAAGAGCATCTCC  
ATAGTGAT 495

Qy 791 CATGAAATTGTGTGAAAGATGAGATATGTA--  
ATGCGTGAGGTACTAAATGAGGATATGT 848

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Db 494  
AATGAGATTGTGTGAAAGATGAGATATGGAGGATATGTGAGGTGCTAAATGA  
GCATCTGT 435

Qy 849  
TAACGAATCGTTTAAGTGGTGATGACCAATGAAGGAATAGGTATAAATAGAG  
ATACTTCA 908

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Db 434  
TAACGAATCGTTTAAGTAGTGATGACTGATAGAGGAACGGGTATAAATAGAG  
CTGCTTCA 375

Qy 909  
ACTATATGCCTTTGAGAATATGTCTTTATTCCTTCCCTTCCTGTTAAGCTTATA  
TCAGCA 968

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Db 374  
ACTGTATGCTTTTGAGAATATATCTTTATTTCTTTCTTTCCTGTTAAGCTTATA  
CCAGCA 315

Qy 969 CTAACAAACAAAACAAATACAATGGTCAAATTA 1001

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Db 314 CTAACAAACAAAACAAATACAATGGTCAAATTA 282